PCT09

RAW SEQUENCE LISTING   DATE: 05/08/2002
PATENT APPLICATION: US/09/807,512   TIME: 13:30:28

Input Set : A:\seqlist_0652.2200000-text.txt
Output Set: N:\CRF3\05082002\I807512.raw

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  5 <110> APPLICANT: Schrier, Peter I.
  6        Aarnoudse, Corlien
  7        Heider, Karl-Heinz
  8        Klade, Christoph
 10 <120> TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
 11        Antigen-Lage 1
 13 <130> FILE REFERENCE: 0652.2200000
 15 <140> CURRENT APPLICATION NUMBER: 09/807,512
 16 <141> CURRENT FILING DATE: 2001-04-16
 18 <150> PRIOR APPLICATION NUMBER: PCT/EP99/07832
 19 <151> PRIOR FILING DATE: 1999-10-15
 21 <150> PRIOR APPLICATION NUMBER: EP 98119583.7
 22 <151> PRIOR FILING DATE: 1998-10-16
 24 <160> NUMBER OF SEQ ID NOS: 28
 26 <170> SOFTWARE: PatentIn Ver. 2.1
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 679
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Homo sapiens
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 35 <221> NAME/KEY: 3'UTR
 36 <222> LOCATION: (340)..(679)
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 40 <222> LOCATION: (1)..(9)
 42 <220> FEATURE:
 43 <221> NAME/KEY: CDS
 44 <222> LOCATION: (10)..(339)
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     51                1                 5                       10
     53     cag ggg gca atg ctg gcg gcc cag gag agg cgg gtg cca cgg gcg gca       96
     54     Gln Gly Ala Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala
     55          15                  20                  25
     57     gag gtc ccc ggg gcg cag ggg cag caa ggg cct cgg ggc cga gag gag      144
     58     Glu Val Pro Gly Ala Gln Gly Gln Gln Gly Pro Arg Gly Arg Glu Glu
     59       30                  35                  40                  45
     61     gcg ccc cgc ggg gtc cgc atg gcg gtg ccg ctt ctg cgc agg atg gaa      192
     62     Ala Pro Arg Gly Val Arg Met Ala Val Pro Leu Leu Arg Arg Met Glu
     63                      50                  55                  60
     67     ggt gcc cct gcg ggg cca gga ggc cgg aca gcc gcc tgc ttc agt tgc      240
     68     Gly Ala Pro Ala Gly Pro Gly Gly Arg Thr Ala Ala Cys Phe Ser Cys
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69                    65                  70                  75
71      aca tca cga tgc ctt tct cgt cgc cca tgg aag cgg agc tgg tcc gca      288
72      Thr Ser Arg Cys Leu Ser Arg Arg Pro Trp Lys Arg Ser Trp Ser Ala
73              80                  85                  90
75      gga tcc tgt ccc ggg atg ccg cac ctc tcc ccc gac cag ggg cgg ttc      336
76      Gly Ser Cys Pro Gly Met Pro His Leu Ser Pro Asp Gln Gly Arg Phe
77          95                  100                 105
79      tga aggacttcac cgtgtccggc aacctactgt ttatccgact gactgctgca           389
82      gaccaccgcc aactgcagct ctccatcagc tcctgtctcc agcagctttc cctgttgatg     449
84      tggatcacgc agtgctttct gcccgtgttt ttggctcagg ctccctcagg gcagaggcgc     509
86      taagcccagc ctggcgcccc ttcctaggtc atgcctcctc ccctagggaa tggtcccagc     569
88      acgagtggcc agttcattgt gggggcctga ttgtttgtcg ctggaggagg acggcttaca     629
90      tgtttgtttc tgtagaaaat aaagctgagc tacgaaaaaa aaaaaaaaaa                 679
94  <210> SEQ ID NO: 2
95  <211> LENGTH: 109
96  <212> TYPE: PRT
97  <213> ORGANISM: Homo sapiens
99  <400> SEQUENCE: 2
101     Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu Met Ala Gln Gly Ala
102       1               5                  10                  15
104     Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala Glu Val Pro
105                 20                  25                  30
107     Gly Ala Gln Gly Gln Gln Gly Pro Arg Gly Arg Glu Glu Ala Pro Arg
108             35                  40                  45
110     Gly Val Arg Met Ala Val Pro Leu Leu Arg Arg Met Glu Gly Ala Pro
111         50                  55                  60
113     Ala Gly Pro Gly Gly Arg Thr Ala Ala Cys Phe Ser Cys Thr Ser Arg
114       65                  70                  75                  80
116     Cys Leu Ser Arg Arg Pro Trp Lys Arg Ser Trp Ser Ala Gly Ser Cys
117                 85                  90                  95
119     Pro Gly Met Pro His Leu Ser Pro Asp Gln Gly Arg Phe
120                 100                 105
124 <210> SEQ ID NO: 3
125 <211> LENGTH: 767
126 <212> TYPE: DNA
127 <213> ORGANISM: Homo sapiens
129 <220> FEATURE:
130 <221> NAME/KEY: CDS
131 <222> LOCATION: (54)..(596)
133 <220> FEATURE:
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135 <222> LOCATION: (597)..(767)
137 <220> FEATURE:
138 <221> NAME/KEY: 5'UTR
139 <222> LOCATION: (1)..(53)
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C--> 143    atcctcgtgg gccctgacct tctctctgag agccgggcag aggctccgga gcc atg     56
144                                                                    Met
145                                                                      1
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147    cag gcc gaa ggc cag ggc aca ggg ggt tcg acg ggc gat gct gat ggc    104
148    Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly
149              5                   10                  15
151    cca gga ggc cct ggc att cct gat ggc cca ggg ggc aat gct ggc ggc    152
152    Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly
153              20                  25                  30
155    cca gga gag gcg ggt gcc acg ggc ggc aga ggt ccc cgg ggc gca ggg    200
156    Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly
157          35                  40                  45
159    gca gca agg gcc tcg ggg ccg aga gga ggc gcc ccg cgg ggt ccg cat    248
160    Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro His
161     50                  55                  60                  65
163    ggc ggt gcc gct tct gcg cag gat gga agg tgc ccc tgc ggg gcc agg    296
164    Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala Arg
165                  70                  75                  80
167    agg ccg gac agc cgc ctg ctt cag ttg cac atc acg atg cct ttc tcg    344
168    Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe Ser
169                  85                  90                  95
171    tcg ccc atg gaa gcg gag ctg gtc cgc agg atc ctg tcc cgg gat gcc    392
172    Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp Ala
173              100                 105                 110
175    gca cct ctc ccc cga cca ggg gcg gtt ctg aag gac ttc acc gtg tcc    440
176    Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val Ser
177          115                 120                 125
179    ggc aac cta ctg ttt atc cga ctg act gct gca gac cac cgc caa ctg    488
180    Gly Asn Leu Leu Phe Ile Arg Leu Thr Ala Ala Asp His Arg Gln Leu
181    130                 135                 140                 145
183    cag ctc tcc atc agc tcc tgt ctc cag cag ctt tcc ctg ttg atg tgg    536
184    Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp
185                  150                 155                 160
187    atc acg cag tgc ttt ctg ccc gtg ttt ttg gct cag gct ccc tca ggg    584
188    Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Ala Pro Ser Gly
189                  165                 170                 175
191    cag agg cgc taa gcccagcctg gcgccccttc ctaggtcatg cctcctcccc    636
192    Gln Arg Arg
193                  180
195    tagggaatgg tcccagcacg agtggccagt tcattgtggg ggcctgattg tttgtcgctg    696
197    gaggaggacg gcttacatgt ttgtttctgt agaaataaa gctgagctac gaaaaaaaaa    756
199    aaaaaaaaaa a                                                       767
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204 <211> LENGTH: 180
205 <212> TYPE: PRT
206 <213> ORGANISM: Homo sapiens
208 <400> SEQUENCE: 4
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211     1               5                   10                  15
213    Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
214                  20                  25                  30
216    Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
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217              35                40                45
219     Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro
220          50                55                60
222     His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala
223      65                70                75                80
225     Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe
226                  85                90                95
228     Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp
229               100               105               110
231     Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val
232          115               120               125
234     Ser Gly Asn Leu Leu Phe Ile Arg Leu Thr Ala Ala Asp His Arg Gln
235          130               135               140
237     Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
238     145               150               155               160
241     Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Ala Pro Ser
242                  165               170               175
244     Gly Gln Arg Arg
245                  180
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250 <211> LENGTH: 993
251 <212> TYPE: DNA
252 <213> ORGANISM: Homo sapiens
254 <220> FEATURE:
255 <221> NAME/KEY: 5'UTR
256 <222> LOCATION: (1)..(55)
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259 <221> NAME/KEY: CDS
260 <222> LOCATION: (56)..(688)
262 <220> FEATURE:
263 <221> NAME/KEY: 3'UTR
264 <222> LOCATION: (689)..(993)
266 <400> SEQUENCE: 5
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269                                                                      Met
270                                                                        1
272     cag gcc gaa ggc cag ggc aca ggg ggt tcg acg ggc gat gct gat ggc        106
273     Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly
274               5                10                15
276     cca gga ggc cct ggc att cct gat ggc cca ggg ggc aat gct ggc ggc        154
277     Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly
278          20                25                30
280     cca gga gag gcg ggt gcc acg ggc ggc aga ggt ccc cgg ggc gca ggg        202
281     Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly
282          35                40                45
284     gca gca agg gcc tcg ggg ccg aga gga ggc gcc ccg cgg ggt ccg cat        250
285     Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro His
286      50                55                60                65
288     ggc ggt gcc gct tct gcg cag gat gga agg tgc ccc tgc ggg gcc agg        298
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289     Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala Arg
290                      70                  75                  80
292     agg ccg gac agc cgc ctg ctt cag ttg cac atc acg atg cct ttc tcg    346
293     Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe Ser
294                      85                  90                  95
296     tcg ccc atg gaa gcg gag ctg gtc cgc agg atc ctg tcc cgg gat gcc    394
297     Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp Ala
298                     100                 105                 110
300     gca cct ctc ccc cga cca ggg gcg gtt ctg aag gac ttc acc gtg tcc    442
301     Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val Ser
302              115                 120                 125
304     ggc aac cta ctg ttt atg tca gtt cgg gac cag gac agg gaa ggc gct    490
305     Gly Asn Leu Leu Phe Met Ser Val Arg Asp Gln Asp Arg Glu Gly Ala
306     130                 135                 140                 145
308     ggg cgg atg agg gtg gtg ggt tgg ggg ctg gga tcc gcc tcc ccg gag    538
309     Gly Arg Met Arg Val Val Gly Trp Gly Leu Gly Ser Ala Ser Pro Glu
310                     150                 155                 160
312     ggg cag aaa gct aga gat ctc aga aca ccc aaa cac aag gtc tca gaa    586
313     Gly Gln Lys Ala Arg Asp Leu Arg Thr Pro Lys His Lys Val Ser Glu
314              165                 170                 175
316     cag aga cct ggt aca cca ggc ccg ccg cca ccc gag gga gcc cag gga    634
317     Gln Arg Pro Gly Thr Pro Gly Pro Pro Pro Pro Glu Gly Ala Gln Gly
318              180                 185                 190
320     gat ggg tgc aga ggt gtc gcc ttt aat gtg atg ttc tct gcc cct cac    682
321     Asp Gly Cys Arg Gly Val Ala Phe Asn Val Met Phe Ser Ala Pro His
322              195                 200                 205
324     att tag ccgactgact gctgcagacc accgccaact gcagctctcc atcagctcct    738
325     Ile
326     210
328     gtctccagca gctttccctg ttgatgtgga tcacgcagtg ctttctgccc gtgttttttgg    798
330     ctcaggctcc ctcagggcag aggcgctaag cccagcctgg cgccccttcc taggtcatgc    858
332     ctcctcccct agggaatggt cccagcacga gtggccagtt cattgtgggg gcctgattgt    918
334     ttgtcgctgg aggaggacgg cttacatgtt tgtttctgta gaaaataaag ctgagctacg    978
336     aaaaaaaaaa aaaaa                                                     993
338  <210> SEQ ID NO: 6
339  <211> LENGTH: 210
340  <212> TYPE: PRT
341  <213> ORGANISM: Homo sapiens
343  <400> SEQUENCE: 6
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346      1               5                  10                  15
348     Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
349                      20                  25                  30
350     Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
351              35                  40                  45
353     Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro
354              50                  55                  60
356     His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala
357     65                  70                  75                  80
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